

052777-sequence\_listing.txt  
SEQUENCE LISTING

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<110> Ikeda, Keiko
<120> Cytoplasmic Polyhedrosis Virus Protein Complex of a Polyhedrin
and a VP3 Polypeptide
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<140> 10/541752
<141> 2006-02-07
<150> PCT/JP2004/000032
<151> 2005-07-10
<160> 2
<170> PatentIn version 3.5
<210> 1
<211> 3259
<212> DNA
<213> Bombyx mori cytoplasmic polyhedrosis virus (strain H)

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<213> Bombyx mori cytoplasmic polyhedrosis virus (strain H)  
<400> 2

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35 40 45

His Thr Leu Arg Leu Leu Gly Pro Phe Gln Tyr Phe Asn Phe Ser Glu  
50 55 60

Thr Asp Arg Gly His Pro Leu Phe Arg Leu Pro Leu Lys Tyr Pro Ser  
65 70 75 80

Lys Ala Ile Pro Ala Asp Glu Leu Ile Asp Asn Leu His Ser Trp Met  
85 90 95

Arg Ser Val His Leu Leu His Val Arg Ser Glu Asp Asn Thr Leu Arg  
100 105 110

Tyr Asn Trp Met Leu Gly Val Tyr Ala Arg Ser Thr Asn Tyr Thr Thr  
115 120 125

Pro Val Gly Gln Leu Val Val Asn Ala Pro Ala Ile Leu Asn Tyr Ser  
130 135 140

Asn Pro Gln Asp Ala Phe Asn Ser Val Phe Val Ala Leu Gly Ile Asp  
145 150 155 160

Tyr Ile Asp Ile Pro Ile Thr Asn Ser Asn Ile Phe Asp Asp Ser Ser  
165 170 175

Thr Pro Tyr Asn Val Arg Ile Trp His Ala Pro Thr Met Thr Glu Val  
180 185 190

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Asn His Ile Leu Ala Leu Met Arg Lys Ser Thr Leu Val Ser Thr His  
195 200 205

Ser Ser Trp His Trp Asp Val Leu His Thr Phe His Tyr Arg Ser Glu  
210 215 220

Ser Asp Met Ile Asp His Phe Ala Ala Lys Ile Leu Glu Asp Trp Arg  
225 230 235 240

Gln Lys Glu Lys Leu Asp Lys Gly Ala Leu Val Glu Ala Asp Arg Val  
245 250 255

Val Gln Arg Leu Ile Pro Leu Ser Ser Ser Thr Tyr Val Gln Arg Leu  
260 265 270

Ala Ala Ile Gly Ala Leu Tyr Pro Asn Glu Phe Thr Glu Asn Val Leu  
275 280 285

Asp Leu Ser Arg Leu Ser Thr Ala Leu Leu Gln Leu Ser Asp Thr Tyr  
290 295 300

Tyr Gln His Ala Asn Asp Gln Leu Arg Arg Leu Tyr Arg Arg Met Tyr  
305 310 315 320

Asn Asp Ser Arg Thr Leu Tyr Met Thr Gln Arg His Gln Glu Leu Leu  
325 330 335

Leu Ala Gln Ile Thr Ala Asp Pro Asn Ile Leu Leu Tyr Pro Tyr Thr  
340 345 350

Tyr Ile Phe Thr Thr Ala Tyr Thr Ser Met Asn Tyr Ile Ser Asn Thr  
355 360 365

Gly Gln Gly Arg Ile Lys His Ser Leu Ala Val Thr Gly Thr Thr Glu  
370 375 380

His Thr Ile Ala Asp Ile Thr Leu Gly Pro Met Ser Glu Asp Val Val  
385 390 395 400

Thr Ile Ser Met Val Glu Pro Met Ser Ile Ala Ala Glu Asp Met Tyr  
405 410 415

Gly Tyr Val Leu Asp Thr Pro Thr Arg Asp Ile Trp Pro Ala Asp Glu  
420 425 430

435

440

445

Ser Arg Ala Leu Gly Met Phe Asn Asn Thr Val Arg Ile Asp Asp Leu  
 450 455 460

Leu Ser Pro Leu Leu Gly Leu Val Tyr Arg Thr Tyr Ile Lys Gly Asp  
 465 470 475 480

Thr Met Thr Met Thr Gln Gly Ser Leu Asp His Leu Thr Leu Cys Ala  
 485 490 495

Ala Val Asp Ser Asp Ile Thr Phe Val Gly Asn Arg Met Ile Ala Pro  
 500 505 510

Leu Ala Glu Gly Tyr Ile Pro Lys Ala Met His Arg Asn Asn Ser Thr  
 515 520 525

Met Lys Met Leu Ser Leu Tyr Val Ala Leu Lys Lys Leu Glu Asn Phe  
 530 535 540

Thr Thr Asn Ser Tyr Leu Met Ala Pro Asp Thr Ser Ile Ile Leu Leu  
 545 550 555 560

Gly Ala Glu Arg Glu Pro Ala Val Ser Ile Leu Arg Arg Phe Asn Arg  
 565 570 575

Ser Val Ser Asn Val Arg Ile Ile Gly Met Gly Asp Arg Ala Val Glu  
 580 585 590

Pro Asn Ile Arg Val Arg Val Pro Phe Pro Ile Asp Lys Asn Ile Ser  
 595 600 605

Ala Asp Phe Ile Ile Cys Asp Ile Asn Ser Tyr Glu Asp Gln Ser Phe  
 610 615 620

Glu Ser Met Phe Gly Glu Thr Ile Ser Val Val Thr Thr Cys Ala Ser  
 625 630 635 640

Ala Ala Thr Arg Val Leu Val Lys Ile Asn His Pro Ser Glu Tyr Met  
 645 650 655

Ile Asn Ser Val Ile Glu Arg Leu Ser Gln Leu Gly Gly Val Phe Tyr  
 660 665 670

His Thr Ala Leu Leu Lys Thr Ala Ser Gln Asn Pro Tyr Ser Tyr Glu  
 675 680 685

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Thr Tyr Ile Tyr Ile Thr Pro Ile Ala Ala Ala Val Arg Phe Pro Phe  
690 695 700

Tyr Ser Asn Ser Ala Ile Ile Asn Arg Tyr Met Thr Ala Val Ala Asp  
705 710 715 720

Asp Glu Thr Pro Ile Ile Pro Ser Ile His Thr Val Ile Lys Gly His  
725 730 735

Ser Asn Thr Tyr Ser Pro Gly Leu Phe Cys Gly Cys Ile Asp Val Gln  
740 745 750

Ser Ala Pro Phe Ala Leu Ser Gln Leu Lys Ser Tyr Cys Ser Glu Ala  
755 760 765

Thr Thr Trp Arg Val Asp Ser Asp Asp Asn Leu Val Asn Ile Ile Ala  
770 775 780

Arg Ile Asp Pro Ala Arg Ile Ala Leu Glu Phe Arg Thr Arg Ser Asn  
785 790 795 800

Thr Ser Ala Tyr His Glu Tyr Gln Arg Tyr Val Pro Asn Gly Leu Gly  
805 810 815

Phe Lys Gly Arg Lys Thr Arg Glu Phe Arg Tyr Ile His Arg Glu Val  
820 825 830

Thr Phe Ile His Lys Leu Met Thr Tyr Ala Leu Ile Arg Glu Gln Ile  
835 840 845

Ser Leu Thr Glu Asn Met Thr Gln Val Val Ser Ile Gly Gly Arg Asn  
850 855 860

Leu Ala Asp Ile Ser Val Val Pro Leu Asn Met Lys Tyr Val Val Ile  
865 870 875 880

Asp Pro Ala Thr Arg Ile Glu Thr Leu Thr Gln Glu Lys Lys Asn Ile  
885 890 895

Glu Val Gln Ser Arg Pro Phe Ser Phe Asp Ala Ala Ser Met Asp Leu  
900 905 910

Glu Asn Asn Ser Ile Tyr Leu Phe Ile Ala Val Ile Met Asn Glu Pro  
915 920 925

Asn Gly Ala Ala Thr Pro Ala Arg Thr Gln Met Asp Lys Ile Arg Asn  
930 935 940

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Val Ala Thr Ala Met Leu Thr Arg Thr Asn Cys Val Ala Tyr Ile Ser  
945 950 955 960

Phe Tyr Glu Ala Gly Ile Ile Thr Arg Leu Asp Gln Ser Thr Ala His  
965 970 975

Lys Thr Ile Arg Val Glu Glu Gly Arg Leu Lys Val Ala Asn Tyr Val  
980 985 990

Pro Val Asp Thr Leu Val Glu Ala Asp Val Thr Leu Met Leu Arg Asp  
995 1000 1005

Ile Gly Ile Thr His Glu Ile Ile Arg Pro Ser Thr Pro Glu Leu  
1010 1015 1020

Ile Asn Ala Cys Ser Asn Tyr Gly Ile Arg Leu Gly Ser Thr Gly  
1025 1030 1035

Gly Ala Val Leu Asp Val Phe Asn His Tyr Ser Pro Val Ile Lys  
1040 1045 1050

Leu Val Arg Ser  
1055